

31 ATGGCCAACAAGCTGAGCAAATCGAACGCCATCGAATGGGCCACGCCACCGGCACAGTACCGCTCCTGGAAAGGAGCTGCTGCCACAGC
 1 M A N K L R R S N A I E W A T A T G T V P L L E R S C C H S

91 GAGGACGCCACTGGAGCCCCAAGCGAGCAAACCCAGCCATAGAGAACAGCCCCATCTGCCACCTGAGGCCACTGAGGCCACCTG TM
 31 E D A A L E P Q A S K T S H R E Q A P I L R H L S Q L S H L

181 CTCATCATGCCGGACTGCTGATCGCTCTTGGGGCGTGACGGAGGGCCGGCATGCCGCTATGTCGAGGAGTCCGACACG
 61 L I I A G L L I V C L A G V T E G R R H A P L M . F E E S D T

271 GGCAGGGGTTCAACCGACCAGCGGTACCGAATGCCAGTTCGCAAAGTTGGGTCCACCTGGTATGCCATTGGT
 91 G R R S N R P A V T E C O F G K V L R E L G S T W Y A D L G

361 CCACCCCTGGAGTTATGTAUTGCATCAAGTGTGAATGTCGCCATACCAAGAACAGCGCGCATGTTGACCGCCAGTGTGCAAT CR1
 121 P P F G V M Y C I K C E C V A I P K K R R I V A R V Q C R N

451 ATCAAAAACGAGTGCCCGCCGAAATGCGATGATCCCATCTCGTTCCCGAAATGCTGCAAGACCTGTCCCGCGATCGAACAGT
 151 I K N E C P P A K C D D P I S L P G K C C K T C P G D R N D

541 ACGGATGTAGCCTGGATGTGCCGTGCCAATGAAGAGGAAGAGCGCAACATGAAACATTACGCTGCGTTGCTAACGGCCGACCTCC
 181 T D V A L D V P V P N E E E E E R N M K H Y A A L L T G R T S

631 TATTTCTCAAGGGTGAGGAATGAAGTCCATGTACACCACCTACAAATCCGCAAGAATCTGCTGGCCACCGCCGTTCTGTTCCACAAG
 211 Y F L K G E E M K S M Y T T Y N P Q N V V A T A R F L F H K

721 AAGAACATATACTACTCTTCTACACCTCATCGGAATCGGTCTCCCGTGCCATTCAATTCTGATGATGCGGGTGTAAATCTGGAG
 241 K N L Y Y S F Y T S S R I G R P R A I Q F V D D A G V I L E

811 GAGCATCAACTGGAGGACCACTGGGGCACTCTAGTCTATCAGAACGCCACGGCAAGATCTGA
 271 E H Q L E T T L A G T L S V Y A N A T G K I STOP

FIGURE 1

1 ATGGCCAACTAGCTGAGGAATCGAACGCCATCGAATGGCCACGGCACAGTACCGCTCCTGAAAGGAGCTGCTGCCACAGC
 1 M A N K L R K S N A I E W A T A T G T V P L L E R S C C H S

91 GAGGACGCCCACTGGAGCCCCAAGCGAGCAAACCGCCATAGAGAACAGCCCCATCTGCCACCTGAGCCAATGCCACCTG
 31 E D A A L E P Q A S K T S H R E Q A P I L R , H L S , Q L S H L TM

181 CTCATCATGCCGGACTGCTGATCGTCTGGCGGGCGTGACGGAGGGCCGCCGATGCCGCTCATGTTGAGGGAGTCGACAGC
 61 L I I A G L L I V C L A G V T E G R R H A P L M F E E S D T

271 GGCAGGCGGTCCAACCGACCAGCGGTACCGAATGCCAGTTGGCAAAGTTGGCGAATTGGGTCACCTGGTATGCCATTGGG
 91 G R R S N R P A V T E C Q F G K V L R E L G S T W * A D L G

361 CCACCCCTCGGAGTTATGTAATGCATCAAGTGTGAATGTCGCAATACCCAAAGAACGGCGCATCGTGCACCGTCCAGTGTGCAAT
 121 P P F G V M Y C I K C E C V A I P K K R R I V A R V Q C R N CR1

451 ATCAAAAACGAGTGCCTGGCCAAATGGATGATGCTCTCGTGGCCGGAAAATGCTGCAAGACCTGTCGGCGATCGAAACGAT
 151 I K N E C P R A K C D D P I S L P G K C C K T C P G D R N D

541 ACGGATGTAGCTTGGATGTGCCGTGCCAATGAAGAGGAAGACCGAACATGAAACATTACGCTGGCTGCTAACGGGCCACCTCC
 181 T D V A L D V P V P N E E E E R N M K H Y A A L L T G R T S

631 TATTTCTCAAGGGTGAGGAATGAAGTCCATGTACACCCCTACAATCGCAGAATCTGGTGGCCACCGCCGTTCTGTTCCACAG
 211 Y F L K G E E M K S M Y T T Y N P Q N V V A T A R F L F H K

721 AAGAATCTATACTACTCCCTCATACCTCATCGCAATCGTCCGTGCCATTCAATTGTTGATGATGCGGGGTAAATCTGGAG
 241 K N L Y Y S F Y T S S R I G R P R A I O F V D D A G V I L E

811 GAGCATCAACTGGAGACCACCTGGCGGGCACTCTCAGTGTCTATCAGAACGCCACGGCAAGATCGGCCGGCTCGAGGGTACCTCTA
 271 E H Q L E T T L A G T L S V Y A N A T G K I G R G S R V P L pUAS Sequences

901 GAGGATTTCTGAAGGAACCTTACTCTGCTGTGACATAATTGACAAACTACCTACAGAGATTAAAGCTCTAA
 301 E D L C E G T L L L W C D I I G N T T Y R D L R L STOP

FIGURE 2

C cont'd

1 ATGGCCAACAAGCTGAGGAAATCGAACGCCATCGAATGGCCACGGCACAGTACCGCTCTGGAAAGGAGCTGCTGCCACAGC
 1 M A N K L R K S N A I E W A T A T G T V P L L E R S C C H S

91 GAGGACGCCCACTGGAGGCCAAGCGAGCAAACAGCCATAGAGAACAGCCCCATCTGCACCTGAGCCACTGAGCCACCTG TM
 31 E D A R A L E P Q A S K T S H R E Q A P I L R H L S Q L S H L

181 CTCATCATCGCCGACTGCTGATCGTCTGCTTGGCGGCGTGACGGAGGGCCGCCGATGCGCCGCTATGTTGAGGAGTCCGACACG
 61 L I I A G L I V C L A G V T E G R R H A P L M F E E S D T

271 GGCAGCGGTCCAACCGACCGGGTACCGAATGCCAGTTGCAAGTTGCGGAATTGGGTCACCTGATGGGATTTGGGT
 91 G R R S N R P A V T E C Q F G K V L R E L G S T W Y A D L G

361 CCACCCCTCGGAGTTATGACTGCATCAAGTGTGAATGTGCGCATACCAAGAAGCGGCGATCGTGCAGTGTGCACAT CRI:W>A
 121 P P F G V M Y C I K C E C V A I P K K R R I V A R V Q C R N

451 ATCAAAAACGACTGGCCGCCAAATGCCATGCCATCTCGTGGCGAAATGCTGCAAGACCTGTCCCGCGATCGAAACGAT
 151 I K N E C P P A K C D N P I S L P G K C C K T C P G D R N D

541 ACGGATGTAGCCTGGATGTGCCGTGCCAATGAGAGAAAGAGCGAACATGAAACATTACGCTGCGTTGCTAACGGCCGACCTCC
 181 T D V A L D V P V P N E E E E R N M K H Y A A L L T G R T S

631 TATTTCTCAAGGGTGGAGAAATGAAGTCCATGTACACCCACTACAATCCGAGAATCTGGTGGCACCCGGTTCTGTTCCAAG
 211 Y F L K G E E M K S M Y T T Y N P Q N V V A T A R F L F H K

721 AAGAAATCTATACTACTCCTCTACACCTCATCGCAATCGTCCGCTGCCATTCAATTGTTGATGATGCGGGTGTAAATCCTGGAG
 241 K N L Y Y S F Y T S S R I G R P R A I Q F V D D A G V I L E

811 GAGCATCAACTGGAGACCACTTGGCGGGACTCTCAGTGTCTATCAGAACATGCCAGGGCAAGATCGCCGCGCTCGAGGGTACCTCTA
 271 E H Q L E T T L A G T L S V Y A N A T S K I G R G S R V P L

901 GAGGATCTTGTGAAGGAACCTTACTCTGTGGTGTGACATAATTGACAAACTACCTACAGAGATTAAAGCTCTAA
 301 E D L C E G T L L L W C D I I G N T T Y R D L K L STOP } pUAS Sequences

FIGURE 3

C cont'd

1 ATGGCCNACAAGCTGAGGAATCGAACGCCATCGAATGGGCCACGGCCACACTACCGCTCTGGAAAGGAGCTGCTGCCACAGC
 1 M A N K L R K S N A I E W A T A T G T V P L L E R S C C H S

91 GAGGACGCCGCACGGAGCCCCAAGCGAGCAAACAGCCATAGAGAACAGCCCCCATCCCTGCCACCTGAGCCAACGTGACCCACCTG TM
 31 E D A A L E P Q A S K T S H R E Q A P I L R H L S Q L S H L

181 CTCATCATGCCGGACTGCTGATCGTCTGGCGGGCTGACGGAGGGCCGCCATGCCGCTCATGTTGAGGAGTCCGACACG
 61 L T I A G L L I V C L A G V T E G R R H A P L M F E E S D T

271 GGCAGGCGGTCCAACCGACCAGGGTCAACCGAACATGCCAGTTGGCAAAGTTTGCGCGATTGGGTCACCTGGTATGCCGATTGGG
 91 G R R S N R P A V T E C Q F G K V L R E L G S T W Y A D L G

361 CCACCCCTCGGAGTTATGTAATGCATCAAGTGTGAATGTTGCGCATACCCAAAGAAGCGGCATCGTTGACCGTCCAGTGTGCAAT
 121 P P F G V M Y C I K C E C V A I P K K R R I V A R V Q C R N

451 ATCAAAAACGACTGCCGGCCAAATGGATGATCATCGTCTGGCCAAATGGATGATCATCGTCTGGCCAAATGGGTCACCTGGGATCGAAACGAT
 151 I K N E C P P A K C D D P * S L P G K C C K T C P G D R N D

541 ACGGATGTAGCCTGGATGTGCCGTGCCAATGAAGAGAAGAGCCAAACATGAAACATTACGCTGCCGTGCTAACGGCCGACCTCC
 181 T D V A L D V P V F N E E E E E R N M K H Y A A L L T G R T S

631 TATTCCTCAAGGGTGAGGAAATGAAGTCCATGTACACCCACCTACAATCGGAGAATCGGTGGCCACGCCGTTCTGTTCCACAAG
 211 Y F L K G E E M K S M Y T T Y N P Q N V V A T A R F L F H K

721 AAGAATCTATACTACTCCTCTACACCTCATCGGAATCGGTGTCGGCTGCCATTCAATTGTTGATGATGCGGGTGTAACTCTGGAG
 241 K N L Y Y S F Y T S S R I G R P R A I Q F V D D A G V I L E

911 GAGCATCAACTGGAGACCACCTGGCCGACTCTCAGTGTCTATCAGAACGGCAAGATCGGCCGGCTCGAGGCAGGCC
 271 E H Q L E T T L A G T L S V Y A N A T G K I G R G S R N R G PUAS/PCR

901 CGCATCTTACCCATACGATGTTCTGACTATGCCCTATCACGTCCCGACTATGCAAGATCCTATCCATATGACCTTCA
 301 R I F [Y P Y D V F D Y A G Y P Y D V P D Y A G S Y P Y D V P

991 GATTACGCTGCTAGTGGCCGCGATTATACGGACGACGACAAATCA
 331 D Y A A N C G R [D Y K D D D D K STOP

} SX-HA
IX-FLAG

FIGURE 4

C cont'd

~~Sequence Range: 1 to 222~~

FIGURE 5

C cont'd

ATATTAGATGGACATGCATAATAATTATTCACTGAACTATGTGATTTTACAGGGTGAAGTCAGAATTAAAATTCTAAAA
 ATTGCAATCAGCGCTTATTGTACATATTATGATGCGATCTCATTATTATTATTATTGATAATATTAGCAGTCGTC
 TCATCAACAAGTATAAAATTGAAATGTTAAAGCAGTCTGGGTTGCCTGCAATGTCGCTGGATCGTGTGCT
 204 DNA site 1
 GCTGATGTTGCCGCGTCGATGTGCCGTTGCAATGTTGCCGCGTTGGCAACTTATAAACACGGAGCGGATCAGTCGTCAGGTC
 TCGCTTGATTCGGGGATGACATCGGCTTCGGCTTTGGGTCGGCATTTAGAGAGATACGATCGATCCGATACGATCCG
 ATCCAGTCAAAATCAAATTCAACCGCACTCCGATCCGTCGCATCATACACGGCGCTCGCACCGCAGTATCTAGTAGATAA
 AAAGTCGCGAGAACGCACTACGGCATATAGCGAAACGCCAAAAAAATAAAGCTCGCTGTCGATCCCTCCTACAGGAT
 CGACTCTATTCCAGGAGCACTAAACACACTAGTGTAAACCATACTATATCTAATCTAATCTAAGGAAACAAAGTCGCAACT
 CGAAAAGCGAATTATGACCGCTAAATAAACGAAACAAAACATAAACACACTATACACATACTACAACTACAAAACAAA
 ATCAAATACATAAATGAGGAATAAAACAGGAAATAGAATAATCCAATAATCGGCGCGGAAACTCGCG
 TGTGTTATCTAATCTGCAAGAGAAGTACAAGAATCGGTATAGAATCGGCTCTACTATCTATACACTGTAATCTATATCATT
 GTGTGTCGCGACTGTGTGCGTGCACCTTGTGTTATATATTGTTGTTGTTCTACTGTGAAACGTGCTTTCAAGCGGTC
 TTCAAAATACAAATACATAACATCAAATCATACACATACATACAGTAAAAACAAAACACATAACATGGCGAAC
 M A N
 1
 AAGCTGAGGAATCGAACCCATCGAATGGGCCACGGCACCGCACAGTACCGCTCTGAAAGGAGCTGCTGCCACAGCGAGGAGGCC
 K L R K S N A I E W A T A T G T V P L L E R S C C H S E D A
 4
 910 GCACTGGAGCCCCAAGCGAGCAAAACAGCCATAGAGAACAGCCCCATCTGCGCCACCTGAGCCAATCTGAGGCCACCTGCTCATC
 34 A L E P Q A S K T S H R E Q A P I L R H L S Q L S H L L I I TM
 1000 GCCGGACTGCTGATCGTCTGCTGGGGCGTGCAGGGAGGGCGCCGATGCGCCGCTCATGTTGAGGAGTCCGACACGGCGAGCG
 64 A G L L I V C L A G V T E G R R H A P L M F E E S D T G R R
 splice
 1090 TCCAAACCGACCAGCGGTACCGAATGCCAGTTGGCAAAAGTTTGCAGGATGGGTCACCTGGTATGCGGATTGGGTCACCC
 94 S N R P A V T E C Q F S K V L R E L G S T W Y A D L G P P F }
 1180 GGAGTTATGACTGATCAAGTGTGAATGTGATGGCATACCAAGAACAGGGCGCATGTTGACGGTCCAGTGTGCAATATCAAAAAC
 124 G V M Y C I K C E C V A I F P K K R F I V A R V Q C R N I K N CR1
 1370 GAGTGCCGCCGCAAATGCGATGATCCCATTGCTGGCCGGAAATGCTGCAAGACCTGTCGGCGATGAAACGATACGGATGTA
 154 E C P P P A R C D D F I S E P G K C C K T C P G D R N D T D V
 1360 GCCTTGGATGTGCCGTGCCAATGAAGAGGAAGAGCGAACATGAAACATTACGCTGCGGTGTAACGGCCGACCTCTATTCTC
 184 A L D V P V P N E E E E R N M K H Y A A L L T G R T S Y F L
 1450 AACGGTGAGGAATGAAGTCCATGTACACCACTACAATCCACAGAATGTGTTGGGCCACCCGGTTCTGTTCCACAAAGAACATCTA
 214 K G E E M K S M Y T T Y N P O N V V A T A R F L F H K K N L
 1540 TACTACTCTCTACACCTCATCGGAATCGGCTCGCGTCCATTCAATCTGTTGATGATGCGGGTAACTCTGGAGCATCAA
 244 Y Y S F Y T S S R I G R P R A I Q F V D D A G V I L E E H Q
 1630 CTGGAGACCACTGGGGCACTCTCAGTGTCTATCAGAATGCCACGGCAAGATCTGCGGTGTCGGCGACAGTCCACGTGATTAC
 274 L E T T L A G T L S V Y Q N A T G K I C G V W R R V P R D Y
 1720 AAGCGCATCCTGCCGACGATCGTCTCCATGTTGTCCTCTCGGGCAACAAACAGCAGGCCAGTTGGCTCTGGCGAAAGGGCC
 304 K R I L R D D R L H V V L L W G N K Q Q A E L A L A G K V A
 1810 AAATACACGGCCCTGAGACGGAGTTGTCAGTCGCTACTGGAGGCCACCTCCGATGGCAAAACGGATCCCCAGCTGGCGAGCC
 334 K Y T A L Q T E L F S S L L E A P L P D G K T D P Q L A G A
 1900 GGTGGCACAGCGATGTGTCACCAGCAGCGGTGCCCTCATGATGCACTCTACCGATGGCTTCATGGTCTTTGGCCGAGGAG
 364 G G T A I V S T S S G A A S S M H L T D V F N G V F G A E E
 1990 TACGGCGATGCAGCACTGAGTGTGAAATTGAGCTGGCAGAACGGAGGAGTGTCTCATGAGATTCACCGTGTGCCAAACCTCT
 394 Y A D A A L S V K I E L A E R K E V I F D E I P R V R K P S
 2080 GCCGAGATCAATGCTCTGGAGCTGTCGCCCCATTCCATACAGAATCTGACTGATGTCGGCTGCAACTCTGCTGACCGTGGAG
 424 A E I N V L E L S S P I S I Q N L R L M S R G K L L L T V E
 2170 TCCAAGAAGTACCCACATCTGCCATCCAGGGACACATCGTACCGAGCCAGCTCGAACTTCACAGACCCCTGCTGGCGCGACAGT
 454 S K K Y P H L R I Q G H I V T R A S C E I F Q T L L A P H S SR1
 2260 GCCGAATCTCGACCAAGAGCAGCGGTTGGCTGGCTACTGAAACACCGATGGATCTCTGGCTACACATCGAAACGGAGCACGTG
 484 A E S S T K S S G L A W V Y L N T D G S L A Y N I E T E H V
 2350 AACACCCGGATAGGCCAACATCAGTTGATTGAGGAGCAGGGCAAGCGGAAGGCCAAGCTGGAGGATCTGAGGCCAGCTCAACTTC
 514 N T R D R P N I S L I E E Q G K R K A K L E D L T P S F N F
 * * *
 2440 AACCGGGCATGGTAGTGGAGAATGGCTCCAAAGTCCTCGAGTCCTGATGCGCCGAACGGCTTAATGGCCACCGAG
 544 N O A I G S V E K L G P K V L E S L Y A G E L G V N V A T E

FIGURE 6

C. caridin

2530 CATGAGACGAGCCTGATCCGTGGCCCTAGTGCCTCGAGTGCCGATGCTGGACTCGGGAAACCATTCTGCTGAAGCGACAG
 574 H E T S L I R G R L V P R P V A D A R D S A E P I L L K R Q

2620 GACACACGGATGCCAGAACATCCACATGCCATGGCGATGGCTGGATGTCATTGACAACGAGTGCAATCTGCACTACGAGGTGACGCTC
 604 E H T D A Q N P H A V G M A W M S I D N E C N L H Y E T L

2710 AACGGTGCCCCGAGGATCTGCAGCTGTATCTGGAGGAGAACCCATCGAGCGATTGGAGGCCAGTGACGAGAAATTGCTCGAG
 634 N G V P A Q D L Q L Y L E E K P I E A I G A P V T R K L L E SR2

2800 GAATTCAACGGCTCTATCTGGAAGGCTCTCCCTAGCATGCCATCCGCCAAGTGTACAGCTGGAGATGAGCTGCTATCTGGAG
 664 E F N G S Y L E G F F L S M P S A E L I K L E M S V C Y L E

2890 GTCCATTCAACGGCACRCCAAACAGCTCTGCTGCCGGAAACTGAAGAGCACCAAGGTGCCGGTCACTGCTTCCCGTCTATACGGAC
 694 V H S K H S K Q L L L R G K L K S T K V P G H C F P V Y T D

2980 AACAAATGTTCCCGTGCCTGGGACCAAAATGATAACCCATTGGTGAACGGAGAGACCAAGTGCTTCACTCCGGACGCTCTACAACGAA SR3
 724 N N V P V P G D H N D N H L V N G E T K C F H S G R F Y N E

3070 TCGGAGCAGTGGCCAGTGGCCAGNATTCTGTCAAGATGTGGCCCTGTTGCGTGGCCAATCCAGTTGCGAGGTGATCAAGTGTCCGGCT CR2

754 S E Q W R S A Q D S C Q M C A C L R G Q S S C E V I K C P A

3160 CTCAGTCAAGTCCACGGAGCAACTGCTCACCGTGTGGTAATGCTGTCAGCTGTGGCCCAAGAAGGGCCCCGACTATTCA
 784 L K C K S T E Q L L Q R B G E C C P S C V P K K E A A D Y S

3250 GCGCAATCTGCCAGCCACCAATGCCACCGATCTGCTCAACAGCGACGCCGGCTGGCGAGCTTCATCCGCCGGTCCC CR3

814 A Q S S P A T N A T D L I Q Q R R G C R L G E Q F H P A G A

3340 AGTTGGCATCATTCTGCCGCCCAATGGCTTCGATAACCTGCAACACCTGCAAGCTGCTGATCCCCTGACCCCTGAGATTGCTGTCCCCGG
 844 S W H P F L P P N G F D T C T T C S C D P L T L E I R C P R

3430 CTCGTCTGCCGCCGTGAGTGAGCGAGAAGTGGCCCTATGTTCCAGACAAGAAGGCATGCTGCAAGATCTGCTGGAGGGCAAGCAG
 874 L V C P P L Q C S E K L A Y R P D K K A C C K I C P E G K Q

3520 AGCAAGTCAATGGACACAAGACGACGCCGAACAATCCAAATGTGTCAGGGATCAGGCCATGCGACGCCAGTCACAGTGCAG
 904 S S S N G H K T T P N N P N V L Q D Q A M Q R S P S H S A E

3610 GAGGTTCTGCCAACGGCGGATGCAAGGTGGTCAACAAAGGTGTACGAGAAAGGCCAGGAGTGGCATTCCGATCTGATGTCCCACGGCAG
 934 E V L A N G G C K V V N K V Y E N G Q E W H P I L M S H G E

3700 CAGAAGTGCATCAAGTGCCTGCAAGGACTCCAAGGTGAAC TGCGATGCCAAGGCTGCTCCCGTCCACGTGCCAGCAGACACGC CR4

964 Q K C T I K C R C K D S K V N C D A K R C S R S T C Q Q Q T R

3790 GTGACCAAGCAAACGGCGTCTGTTGAGAAACGGACGCAGCTGCTCCGCCATCGATGAGTTCTGCTCCACCCAGTGCAGGAGATCGAGG
 994 V T S K R R L F E K P D A A A P A I D E F C S T Q C R R S R

3880 CGCCACACAAAGAGGCAGCGCATCATCAGCAGCGATCTCCAGCTGAGCGCTCACGTGACGGATGGATCCAATCCAGTATCAGAT
 1024 R H H K R Q P H H Q Q R S S S end

3970 CCTTGGCCAGGGAGCGAACCAATCACTCACTCACCACTCACCAACTCAGTGTACTCAGTGTGCAACACACACACACACAC
 4060 ACACACAAACCAACAAACACTCACACCCACATCTACACAGACACACACACAGCCACAAAAGCGAACGCCACACAGACTTGTGCAAGGA
 4150 GTTGCATAGATCGTTGCTATCTTATCATGTGGCAGCAATGAGAACTTGATATTATATATATGAAATCACCGAGGAGAAAACGTAGGAGA
 4240 GAAATCTCACAAAAATATATATATCTTATGGAGGAACCGTAGTAATAGACAGAGAGAGAGAGAGAGAGAGTCTAATGAGATCC
 4330 TTGGAAAAGGACATTAAACCGTAGCTGAGTTGCTTTAAATTCTCCACCGCAGAATTCTATTGAAAGCATTGAAATTCTTTCGC
 4420 AGTTACCCACCCGTGTAACCAATCCCTCCCTCCCAACCAACAAACACCCAAAAAAACTAAAACATTAAATACAATTAA
 4510 ATTTATACAAAACAAAAACAAAAAA

FIGURE 6

C and

TM

- CRI

FIGURE 1

FIGURE 2

TM

CR1:W->A

RJAS Sequences

FIGURE 3

FIGURE 4

~~Sequence Range: 1 to 222~~

10 20 30 40 50 60 70
Met protein M E N S Q C L V T P P A L M / F G L E I D Q G G C H R I R P A P S E N P L V D L I E K P O R T P R K H D I N T I L A T M G F P

Nog protel

Neg protein: HDPPEPLGVEDLGFLMLPQPSGAMPASSEKGLFVEGLASGDFPLSKTLPKIQMWLWSQTFCVLYTWNDLC

SuperSog ? | 300 310 ~~args:RvplEcegtllw>~~ ~~args~~ Vector

Neg protel: **ELPERRLOVEDLGELLLR**

~~180~~ 190 ~~200~~ 210 220

~~Neg. protein: RYVKV/GSC/SKGS/CSVP?EGMUCP?XSMETILPWRQCQ?EVQCN?WTTIQYPT?SECKCSC~~

FIGURE 5

FIGURE 6